

2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
20	GCAATTCGAA	ACCCCAAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTGG	TTGTCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTGAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
25	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCGTTGC	CATTTCTGGT	TTCGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTA	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
30	CTGTCCCAAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
35	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTTCTTGCA	AATTCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
	CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
40	GA					1052

2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

60	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
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    ATGAAGGTAC AGTATCTCTT ACATTAGAAG TGGCATTACA ACTTGGCGAT      100
    GATGTCGTAC  GTACAATTGC AATGGATTCT ACTGATGGTG TTAAACGTGG      150
    TACAGAAAGTT CGAGATAGCG GAGATAGCAT CAGTGTTCCTA GTTGGTGATG      200
    CTACGTTAGG  ACGTGTGTTT AATGTTCTTG GTGATACAAT TGACTTAGAC      250
5   GAGAAGCTTG  ATAATTCTGT CAAACGTGAT CCAATTCATA GAGAAGCACC      300
    TGCATTTCGAT CAATTATCAA CAAAAGTTGA AATCTTAGAA ACAGGTATTA      350
    AAGTAATTGA  TTTACTTGCA CCATATATTA AAGGTGGTAA AATCGGTTTA      400
    TTCGGTGGCG  CTGGTGTAGG TAAAACAGTA TTAATTCAAG AATTAATTAA      450
    TAATATAGCT  CAAGAACATG GTGGTATTTT AGTATTTGCC GCGTAGGTG      500
10  AACGTACGCG  TGAAGGTAAT GACTTATACT ACGAAATGAG TGATAGTGGT      550
    GTTATTAAGA  AAACAGCTAT GGTCTTCGGA CAAATGAATG AGCCACCTGG      600
    TGCGCGTATG  CGTGTGCTT TATCAGGCTT AACAAATGGCT GAACACTTCC      650
    GTGATGTACA  AGGACAAGAT GTTTTACTAT TTATTGATAA CATATTCAGA      700
    TTTACGCAAG  CTGGTTTACA AGTATCAGCA CTATTAGGTC GTATGCCATC      750
15  AGCCGTTGGT  TATCAACCTA CCCTTGCTAC TGAAATGGGT CAATTACAAG      800
    AACGTATTAC  ATCAACAACCT AAAGGATCTG TAACGTC      837

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20 2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

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35  AAGGTATTTCG ATGCCTTGAA AATGGAAGGC TCCGAGCTGA CCCTGGAAGT      50
    ACAACAGCAG  CTGGGCGACG GCATTGTCCG TACCATTGCA CTGGGTACCT      100
    CCGACGGCCT  GCGTCGCGGC ATGATGATCC AGAACACCGG CAAACCTATC      150
    ATGGTGCCAG  TCGGTAAAGC AACCTGGGT CGCATCATGG ACGTGCTGGG      200
40  TAACCCGATC  GACGAATGCG GCGCGGTCGC TCACGACCAG ATCGCTTCGA      250
    TCCACCGCGC  TCCTCCTGCG TACGACGAAC TGTCGCCATC GCAAGATCTG      300
    CTGGAAACCG  GCATTAAAGT TATTGACCTG GTGTGCCCGT TCGCCAAGGG      350
    CCGTAAAGTC  GGTCTGTTCG GCGGTGCAGG TGTGGGCAAG ACCGTGAACA      400
    TGATGGAAC  TATCAACAAC ATCGCCAAAG CACACTCGGG TCTGTCCGTG      450
45  TTTGCCGGTG  TGGGTGAGCG TACCCGTGAA GGTAACGACT TCTACCACGA      500
    GATGGCTGAC  GCCAAAGTGG TCGATCTGGA AAATCCAGAG AACTCCAAGG      550
    TTGCGATGGT  CTACGGTCAG ATGAATGAAC CACCAGGCAA CCGTCTGCGC      600
    GTGGCGCTGA  CCGGTCTGAC CATGGCTGAA GCATTCCGTG ACGAAGGCAA      650
    AGACGTTCTG  TTCTTCGTGG ACAACATCTA CCGCTTCACC CTGGCCGGTA      700
50  CCGAAGTATC  GGCACGTGCT GGCCGTATGC CATCGGCTGT GGGTTACCAG      750
    CCTACGCTGG  CCGAAGAAAT GGGTCGCCTG CAAGAGCGCA TCACTTCGAC      800
    CAAGACCGGT  TCGATCAC      818

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55 2) INFORMATION FOR SEQ ID NO: 868

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

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CTATCTTAGT AGTATCTGCT GCTGATGGCC CAATGCCACA AACTCGTGAA      50
CACATTCTTT TATCACGTAA CGTTGGTGTT CCAGCATTAG TTGTATTCTT      100
AAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTAGAAA      150
TGGAAGTTTCG TGACTTATTA AGCGAATATG ACTTCCCAGG TGACGATGTA      200
CCTGTAATCT CTGGTTCCTGC ATTAAAAGCT TTAGAAGGCG ACGCTGACTA      250
TGAGCAAAAA ATCTTAGACT TAATGCAAGC TGTTGATGAC TTCATTCCAA      300
CACCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT TGAGGACGTA      350
TTCTCAATCA CTGGTCGTGG TACTGTTGCT ACAGGCCGTG TTGAACGTGG      400
TCAAAATCAAA GTCGGTGAAG AAATCGAAAT CATCGGTATG CAAGAAGAAT      450
CAAGCAAAAC AACTGTTACT GGTGTAGAAA TGTTCCGTAA ATTATTAGAC      500
TACGCTGAAG CTGGTGACAA CATTGGTGCA TTATTACGTG GTGTTTCACG      550
TGATGACGTA CAACGTGGTC AAGTTTTAGC TGCTCCTGGT ACTATTACAC      600
CACATACAAA ATTCAAAGCG GATGTTTACG TTTTATCTAA AGATGAAGGT      650
GGTCGTCATA CACCATTCTT CACTAACTAC CGCCCACAAT TCTATTTCCG      700
TACTACTGAC GTAACGTGGT TTGTTAACTT ACCAGAAGGT ACTGAAATGG      750
TTATGCCTGG CGATAACGTT GAAATGGA                                778

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2) INFORMATION FOR SEQ ID NO: 869

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

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TGCTCCTATG CCTCAAACAC GTGAACACAT CTTGTTATCA CGTAACGTTG      50
GTGTACCATA CATCGTTGTT TTCTTAAACA AAATGGATAT GGTGATGAC      100
GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTGTCAGA      150
ATATGACTTC CCAGGCGACG ATGTTCCCTGT AATCGCTGGT TCTGCTTTGA      200
AAGCTCTTGA AGGCGATGCT TCATACGAAG AAAAAATCAT GGAATTAATG      250
GCTGCAGTTG ACGAATACGT TCCAACCTCA GAACGTGACA CTGACAAACC      300
ATTATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG      350
TTGCTACAGG CCGTGTGTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT      400
GAAATCGTTG GTATTGCTGA AGAACTGCT AAAACAACCTG TAACTGGTGT      450
TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG      500
GTGCATTGCT ACGTGGTGTG GCTCGTGAAG ACATCCAACG TGGACAAGTA      550
TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTTA AAGCTGAAGT      600
TTACGTTTTA ACAAAGAAG AAGGTGGACG TCACACTCCA                        640

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2) INFORMATION FOR SEQ ID NO: 870

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 15 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
20	GTACCATACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
25	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACTGTA	ACTGGTGTG	450
	AAATGTTCCG	TAAATTGTGA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
30	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTAAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

35 2) INFORMATION FOR SEQ ID NO: 871

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

50	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTT	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
55	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCTGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACTGTAA	CTGGTGTGTA	450
60	AATGTTCCGT	AAATTGTGTA	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500

CATTGCTACG TGGGGTTGCT CGTGAAGACA TCCAACGTGG ACAAGTATTA 550
 GCTAAAGCTG GTACAATCAC ACCTCATACA AAATTTAAAG CTGAAGTTTA 600
 CGTTTTAACA AAAGAAGAAG GTGGACGTCA CACTCCA 637

5

2) INFORMATION FOR SEQ ID NO: 872

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 643 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

25 GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC 50
 GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA 100
 AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT 150
 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA 200
 GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC 250
 TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGATACT GACAAACCAT 300
 TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT 350
 30 GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA 400
 AATCGTTGGT ATTGCTGACG AAACCTGCTAA AACAACTGTA ACAGGTGTTG 450
 AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT 500
 GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT 550
 GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT 600
 35 ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT CTT 643

2) INFORMATION FOR SEQ ID NO: 873

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

55 GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC 50
 GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA 100
 AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT 150
 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA 200
 GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC 250
 60 TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGATACT GACAAACCAT 300

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TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT 350
GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA 400
AATCGTTGGT ATTGCTGACG AAAGTCTGCTAA AACAAGTGTG ACAGGTGTTG 450
AAATGTTCCG TAAATTGTGA GACTATGCTG AAGCAGGGGA TAACATTGGT 500
5 GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT 550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT 600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC AACTCCATT C 641

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10

2) INFORMATION FOR SEQ ID NO: 874

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: LSPQ 2514

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

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ACCAGCATTG TAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG 50
AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
GACTTCCAGG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC 150
30 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC 250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
TACAGGCCGT GTTGAACGTG GGCAAATCAA AGTTGGTGAA GAAGTTGAAA 350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAAGAAATG 400
35 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT 450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG 500
CTCCAGGTTT AATCACACCT CACACAAAAA TTAAAGCAGA CGTATACGTT 550
TTATCTAAAG ACGAAGGTGG ACCTCACACT CCATTCTTCA CAAACTATCG 600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC 650
40 CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A 681

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45 2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 675 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: R591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

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60 ATTATCACGT AACGTTGGTG TACCAGCATT AGTTGTATTC TTAAACAAAG 50

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TTGACATGGT AGACGACGAA GAATTATTAG AATTAGTTGA AATGGAAGTT 100
CGTGACTIONAT TAAGCGAATA TGACTIONCCA GGTGACGATG TACCTGTAAT 150
CGCTGGTTCT GCATTAAAAG CATTAGAAGG CGATGCTGAA TACGAACAAA 200
AAATCTTAGA CTTAATGCAA GCAGTTGATG ATTACATTCC AACTCCAGAA 250
5 CGTGATTCTG ACAAACCATT CATGATGCCA GTTGAGGACG TATTCTCAAT 300
CACTGGTCGT GGTACTGTTG CTACAGGCCG TGTTGAACGT GGTCAAATCA 350
AAGTTGGTGA AGAAGTTGAA ATCATCGGTA TGCACGAAAC TTCTAAAACA 400
ACTGTTACTG GTGTAGAAAT GTTCCGTAAA TTATTAGACT ACGCTGAAGC 450
TGGTGACAAC ATCGGTGCTT TATTACGTGG TGTTGCACGT GAAGACGTAC 500
10 AACGTGGTCA AGTATTAGCT GCTCCTGGTT CTATTACACC ACACACAAAA 550
TTCAAAGCTG AAGTATACGT ATTATCTAAA GATGAAGGTG GACGTCACAC 600
TCCATTCTTC ACTAACTATC GCCACAATT CTATTTCCGT ACTACTGACG 650
TAACTGGTGT TGTAACCTTA CCAGA 675

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2) INFORMATION FOR SEQ ID NO: 876

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 704 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus epidermidis*
 - (B) STRAIN: CSG 10

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

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TCTTATTATC ACGTAACGTT GGTGTACCAG CATTAGTTGT ATTCTTAAAC 50
AAAGTTGACA TGGTAGACGA CGAAGAATTA TTAGAATTAG TTGAAATGGA 100
35 AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG 150
TAATCGCTGG TTCTGCATTA AAAGCATTAG AAGGCGATGC TGAATACGAA 200
CAAAAAATCT TAGACTTAAT GCAAGCAGTT GATGATTACA TTCCAACCTC 250
AGAACGTGAT TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT 300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA 350
40 ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTATGCACG AAACCTCTAA 400
AACAACGTGT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG 450
AAGCTGGTGA CAACATCGGT GCTTTATTAC GTGGTGTTC ACGTGAAGAC 500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTCTATTA CACCACACAC 550
AAAATTCAAA GCTGAAGTAT ACGTATTATC TAAAGATGAA GGTGGACGTC 600
45 ACACTCCATT CTTCACTAAC TATCGCCAC AATTCTATTT CCGTACTACT 650
GACGTAACTG GTGTTGTAAA CTTACCAGAA GGTACAGAAA TGTTATGCC 700
TGGC 704

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2) INFORMATION FOR SEQ ID NO: 877

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 770 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(B) STRAIN: ATCC 35984

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

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TCTTAGTTGT ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC      50
ATCTTATTAT CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA      100
CAAAGTTGAC ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG      150
10 AAGTTCGTGA CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT      200
GTAATCGCTG GTTCTGCATT AAAAGCATTG GAAGGCGATG CTGAATACGA      250
ACAAAAAATC TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAACCTC      300
CAGAACGTGA TTCTGACAAA CCATTTCATG TGCCAGTTGA GGACGTATTTC      350
TCAATCACTG GTCGTGGTAC TGTTGCTACA GGCCGTGTTG AACGTGGTCA      400
15 AATCAAAGTT GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA      450
AAACAACCTG TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT      500
GAAGCTGGTG ACAACATCGG TGCTTTATTA CGTGGTGTGG CACGTGAAGA      550
CGTACAACGT GGTCAAGTAT TAGCTGCTCC TGGTTCCTATT ACACCACACA      600
CAAAATTCAA AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT      650
20 CACACTCCAT TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC      700
TGACGTAACT GGTGTTGTAA ACTTACCAGA AGGTACAGAA ATGTTTATGC      750
CTGGCGACAA CGTTGAAATG      770

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2) INFORMATION FOR SEQ ID NO: 878

(i) SEQUENCE CHARACTERISTICS:

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30 (A) LENGTH: 716 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(B) STRAIN: ATCC 35983

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

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TTGTATTCTT AAACAAAGTT GACATGGTAG ACGACGAAGA ATTATTAGAA      50
TTAGTTGAAA TGGAAGTTTC TGAATTATTA AGCGAATATG ACTTCCCAGG      100
TGACGATGTA CCTGTAATCG CTGGTTCTGC ATTAAAAGCA TTAGAAGGCG      150
45 ATGCTGAATA CGAACAAAAA ATCTTAGACT TAATGCAAGC AGTTGATGAT      200
TACATTCCAA CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT      250
TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT ACAGGCCGTG      300
TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT CATCGGTATG      350
CACGAAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT TCCGTAAATT      400
50 ATTAGACTAC GCTGAAGCTG GTGACAACAT CGGTGCTTTA TTACGTGGTG      450
TTGCACGTGA AGACGTACAA CGTGGTCAAG TATTAGCTGC TCCTGGTTCT      500
ATTACACCAC ACACAAAATT CAAAGCTGAA GTATACGTAT TATCTAAAGA      550
TGAAGGTGGA CGTCACACTC CATTCTTCAC TAACTATCGC CCACAATTCT      600
ATTTCCGTAC TACTGACGTA ACTGGTGTG TAAACTTACC AGAAGGTACA      650
55 GAAATGGTTA TGCCTGGCGA CAACGTTGAA ATGACAGTTG AATTAATCGC      700
TCCAATCGCT ATCGAA      716

```

60 2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

```

15  CGGTCCTATG CCTCAAATC GTGAACACAT CTTGTTATCA CGTAACGTTG      50
    GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTGATGAC      100
    GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA      150
    ATATGACTTC CCAGGCGACG ATGTTCCCTGT AATCGCCGGT TCTGCTTTGA      200
20  AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG      250
    GCTGCAGTTG ACGAATACGT TCCAACCTCA GAACGTGATA CTGACAAACC      300
    ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG      350
    TTGCTACAGT CCGTGTTGAA CGTGGAACAAG TTCGCGTTGG TGATGAAGTA      400
    GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT      450
25  TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG      500
    GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA      550
    TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTCA AAGCTGAAGT      600
    TTATGTTTTG ACAAAGAAG AAGGTGGACG TCACACTCCA      640

```

2) INFORMATION FOR SEQ ID NO: 880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

```

    CGGCGCGATC CTGGTTTGCT CGGCTGCCGA CGGCCCATG CCGCAGACCC      50
    GCGAGCACAT CCTGCTGTCC CGCCAGGTAG GCGTTCCTTA CATCGTCGTG      100
50  TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TGGAACTGGT      150
    CGAGATGGAA GTTCGCGATC TGCTGAACAC CTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CATCATCGGT TCCGCGCTGA TGGCGCTGGA AGGCAAGGAT      250
    GACAACGGCA TCGGCGTAAG CGCCGTGCAG AAGCTGGTAG AGACCCTGGA      300
    CTCCTACATT CCGGAGCCGG TTCGTGCCAT CGACCAGCCG TTCCTGATGC      350
55  CGATCGAAGA CGTGTTCTCG ATCTCCGGCC GCGGTACCGT GGTAACCGGT      400
    CGTGTAAGAG GCGGCATCAT CAAGGTCCAG GAAGAAGTGG AAATCGTCGG      450
    CATCAAGGCG ACCACCAAGA CTACCTGCAC CGGCGTTGAA ATGTTCCGCA      500
    AGCTGCTCGA CGAAGGTCGT CTGGTGAGA ACGTTGGTAT CCTGCTGCGT      550
    GGCACCAAGC GTGAAGACGT AGAGCGTGGC CAGGTTCTGG CCAAGCCGGG      600
60  CACCATCAAG CCGCACACCA AGTTCGAGTG CGAAGTGTAC GTGCTGTCCA      650

```

AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

5

2) INFORMATION FOR SEQ ID NO: 881

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 642 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
25 ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
30 ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTAATGTTGC	350
TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
35 CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

40 2) INFORMATION FOR SEQ ID NO: 882

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

55 CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
60 TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250

```

CAGTTGACGA ATACGTTCCA ACTCCAGAAC GTGACACTGA CAAACCATTC 300
ATGATGCCAG TCGAAGACGT ATTCTCAATC ACTGGACGTG GTACTGTTGC 350
TACAGGCCGT GTTGAACGTG GACAAGTTTCG CGTTGGTGAC GAAGTTGAAA 400
TCGTTGGTAT TGCTGAAGAA ACTGCTAAAA CAACTGTAAC TGGTGTGAA 450
5 ATGTTCCGTA AATTGTTAGA CTATGCTGAA GCAGGGGATA ACATTGGTGC 500
ATTGCTACGT GGTGTTGCTC GTGAAGACAT CCAACGTGGA CAAGTATTGG 550
CTAAAGCTGG TACAATCACA CCTCATACAA AATTTAAAGC TGAAGTTTAC 600
GTTTTAACAA AAGAAGAAGG TGGACGTCAT ACACCA 636

```

10

2) INFORMATION FOR SEQ ID NO: 883

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R422

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

```

GGTCCTATGC CTCAAACACG TGAACATATC TTATTATCAC GTAACGTTGG 50
TGTACCATAC ATCGTTGTAT TCTTAAACAA AATGGATATG GTTGATGACG 100
30 AAGAATTATT AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCAGAA 150
TACGATTTCC CAGGCGATGA TGTTCCAGTT ATCGCAGGTT CTGCTTTGAA 200
AGCTTTAGAA GGCACGAGT CTTATGAAGA AAAAATCTTA GAATTAATGG 250
CTGCAGTTGA CGAATATATC CCAACTCCAG AACGTGATAC TGACAAACCA 300
TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT 350
35 TGCTACAGGC CGTGTTGAAC GTGGTGAAGT TCGCGTTGGT GACGAAGTTG 400
AAATCGTTGG TATTAAAGAC GAAACATCTA AAACAACGTG TACAGGTGTT 450
GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCAGGCG ACAACATCGG 500
TGCTTTATTA CGTGGTGTAG CACGTGAAGA TATCGAACGT GGACAAGTAT 550
TAGCTAAACC AGCTACAATC ACTCCACACA CAAAATTCAG AGCTGAAGTA 600
40 TACGTATTAT CAAAAGAAGA AGGCGGACGT CACACTCCAT T 641

```

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

```

60 TATGCCTCAA ACACGTGAAC ATATCTTATT ATCACGTAAC GTTGGTGTAC 50

```

```

CATACATCGT TGTATTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA 100
TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAT CAGAATACGA 150
TTTCCCAGGC GATGATGTTC CAGTTATCGC AGGTTCTGCT TTGAAAGCTT 200
TAGAAGGCCA CGAGTCTTAT GAAGAAAAAA TCTTAGAATT AATGGCTGCA 250
5 GTTGACGAAT ATATCCCAAC TCCAGAACGT GATACTGACA AACCATTTCAT 300
GATGCCAGTC GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA 350
CAGGCCGTGT TGAACGTGGT GAAGTTCGCG TTGGTGACGA AGTTGAAATC 400
GTTGGTATTA AAGACGAAAC ATCTAAAACA ACTGTTACAG GTGTTGAAAT 450
GTTCCGTAAA TTATTAGACT ACGCTGAAGC AGGCGACAAC ATCGGTGCTT 500
10 TATTACGTGG TGTTCACGT GAAGATATCG AACGTGGACA AGTATTAGCT 550
AAACCAGCTA CAATCACTCC ACACACAAAA TTCAAAGCTG AAGTATACGT 600
ATTATCAAAA GAAGAAGGCG GACGTCACAC TCCATTCTTC 640

```

15

2) INFORMATION FOR SEQ ID NO: 885

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 632 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Enterococcus faecium
    (B) STRAIN: R492

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

```

TGCCTCAAAC TCGTGAACAC ATCCTATTGT CTCGTCAAGT TGGTGTTCCT 50
TACATCGTTG TATTCTTGAA CAAAGTAGAC ATGGTTGATG ACGAAGAATT 100
ACTAGAATTA GTTGAAATGG AAGTTCGTGA CCTATTAACA GAATACGAAT 150
35 TCCCTGGTGA CGATGTTTCT GTAGTTGCTG GATCAGCTTT GAAAGCTCTA 200
GAAGGCGACG CTTCATACGA AGAAAAAATT CTTGAATTAA TGGCTGCAGT 250
TGACGAATAC ATCCCAACTC CAGAACGTGA CAACGACAAA CCATTTCATGA 300
TGCCAGTTGA AGACGTGTTC TCAATTACTG GACGTGGTAC TGTTGCTACA 350
GGTCGTGTTG AACGTGGACA AGTTCGCGTT GGTGACGAAG TTGAAGTTGT 400
40 TGGTATTGCT GAAGAAACTT CAAAAACAAC AGTTACTGGT GTTGAAATGT 450
TCCGTAAATT GTTAGACTAC GCTGAAGCTG GAGACAACAT TGGTGCTTTA 500
CTACGTGGTG TTGCACGTGA AGACATCCAA CGTGGACAAG TTTTAGCTAA 550
ACCAGGTACA ATCACACCTC ATACAAAATT CTCTGCAGAA GTATACGTGT 600
TGACAAAAGA AGAAGGTGGA CGTCATACTC CA 632
45

```

2) INFORMATION FOR SEQ ID NO: 886

50

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 640 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Enterococcus faecium
    (B) STRAIN: R576

```

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

```

5  CCGCCCAATG CCTCAAAC TC GTGAACACAT CCTATTGTCT CGTCAAGTTG 50
   GTGTTCTTCA CATCGTTGTA TTCTTGAACA AAGTAGACAT GGTGATGAC 100
   GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 150
   ATACGAATTC CCTGGTGACG ATGTTCTCTGT AGTTGCTGGA TCAGCTTTGA 200
   AAGCTCTAGA AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG 250
   GCTGCAGTTG ACGAATACAT CCCAACTCCA GAACGTGACA ACGACAAACC 300
10 ATTCATGATG CCAGTTGAAG ACGTGTTCCTC AATTACTGGA CGTGGTACTG 350
   TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT 400
   GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT 450
   TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCTGGA GACAACATTG 500
   GTGCTTTACT ACGTGGTGTT GCACGTGAAG ACATCCAACG TGGACAAGTT 550
15 TTAGCTAAAC CAGGTACAAT CACACCTCAT ACAAATTCT CTGCAGAAGT 600
   ATACGTGTTG ACAAAGAAG AAGGTGGACG TCATACTCCA 640

```

20 2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 806 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Zoogloea ramigera
   (B) STRAIN: ATCC 25935

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

```

35 ATCCTGGTTT GCTCCGCAGC TGACGGCCCA ATGCCACAGA CCCGCGAGCA 50
   CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCTTGA 100
   ACAAGTGCGA CCTGGTTGAC GACGCAGAAC TGCTGGAAC TGTGAAATG 150
   GAAGTGCGTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC 200
40 AATCATCAAG GGTTCGGCAC GTATGGCGCT TGAAGGCAAA GAAGGCGAGA 250
   TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC 300
   CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA 350
   CGTGTTCCTG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC 400
   GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC 450
45 ACCGTCAAAA CCACTTGAC CCGCGTGGA ATGTTCCGCA AGCTGCTGGA 500
   CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC 550
   GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG 600
   CCGCACAAAC ACTTCACCGG CGAGATCTAC GTTCTGTGCA AAGATGAAGG 650
   CGGCCGTCAC ACCCGTTCT TCAACAATA TCGTCCACAG TTCTACTTCC 700
50 GTACGACTGA CGTGACCGGT TCGATCGAAC TGCCAGCAGA CAAAGAAATG 750
   GTCATGCCAG GCGACAACGT GTCGATCACC GTCAAGCTGA TCAACCCGAT 800
   CGCGAT 806

```

55

2) INFORMATION FOR SEQ ID NO: 888

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 634 bases
   (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: R503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAACAA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAT	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
AAACCAGCTA	CAATCACTCC	ACACACAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
TTGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTAATCGTGA	150
GGGTAAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTGAGCTCG	200
AGGGTGAATC	CAAGGTCGCA	CTGGTGTTCT	GACAGATGAA	CGAGCCCCCC	250
GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
TCTGCCGTCT	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

(i) SEQUENCE CHARACTERISTICS: 890

(A) LENGTH: 466 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

```

10 TTGATTGTAC GTCTTTACCT TTCTGCCTGA CTGTTTACGA CAACTAACGA      50
   AAGCGTAGAA CAACATTGCC AAGGCTCACG GTGGTTACTC TGTCTTCACT      100
   GGTGTCGGTG AACGTACTCG TGAGGGTAAC GATTTGTACC ACGAAATGCA      150
   GGAAACTGGT GTCATTCAGC TCGAGGGTGA ATCCAAGGTC GCCCTCGTGT      200
15 TCGGTCAGAT GAACGAGCCC CCCGGTGCCC GTGCCCCTGT CGCTCTTACT      250
   GGTTTGACCA TTGCCGAGTA CTTCCGTGAC GAGGAAGGTC AGGACGTGCT      300
   TCTCTTCATT GACAACATTT TCCGTTTCAC TCAGGCCGGT TCTGAGGTGT      350
   CTGCCCTTCT GGGTCGTATC CCCTCTGCCG TCGGTTACCA GCCCACCTTT      400
   CCCGTCGACA TGGGTATCAT GCAGGAGCGT ATTACCACCA CCACCAAGGG      450
20 TTCCATCACC TCCGTC                                     466

```

2) INFORMATION FOR SEQ ID NO: 891

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Paecilomyces lilacinus*

(B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

```

40 AGGAGCTGAT CAACAACATC GCCAAGGCTC ACGGTGGTTA CTCCGTCTTC      50
   ACTGGTGTCTG GTGAGCGTAC CCGTGAGGGT AACGATCTGT ACCACGAAAT      100
   GCAGGAGACC TCGGTCATTC AGCTCGAGGG CGAGTCTAAG GTGGCCCTGG      150
   TCTTTGGTCA GATGAACGAG CCCCCGGGTG CTCGTGCCCCG TGTCGCTCTT      200
   ACTGGTCTTA CCGTCGCCGA GTACTTCCGT GACCAGGAGG GTCAGGATGG      250
45 TTAGTTCTCG TCCACTCATG CCGAAACATG TGCGTGTTCC GAGGCTAATC      300
   AACGTGCCAG TGCTGCTTTT CATCGACAAC ATTTTCCGAT TCACACAGGC      350
   CGGTTCCGAG GTGTCTGCCC TGCTGGGTCG TATCCCCTCT GCCGTCGGTT      400
   ACCAGCCAC CCTCGCCGTC GACATGGGTG GCATGCAGGA GCGTATCACC      450
   ACCACCAAGA AGGGCTCTAT CACCTCCG                                     478
50

```

2) INFORMATION FOR SEQ ID NO: 892

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

5 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

	GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
10	TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
	TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
	GTACCACGAA	ATGCAGGAAA	CTGGTGTCAT	TCAGCTCGAG	GGTGAATCCA	200
	AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCCCG	TGCCCGTGCC	250
	CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
15	AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
	CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GATATCCCCTC	TGCCCGTCGGT	400
	TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
	CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

20

2) INFORMATION FOR SEQ ID NO: 893

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1208 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

35 (B) STRAIN: ATCC 14285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

	CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
	CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
40	TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
	GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
	TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCCG	GGTGGTAAGA	250
	TTGGTCTGTT	TGGCGGTGCC	GGTGTGGA	AGACCGTGTT	CATCCAGGAG	300
	CTCATCAACA	ACATCGCCAA	GGCCACGGT	GGTACTCCG	TCTTCACCGG	350
45	TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
	AGACCTCTGT	CATTAGCTT	GACGGTGA	CCAAGGTCGC	CCTGGTGTTT	450
	GGTCAGATGA	ACGAGCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
50	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCGCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
55	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCGA	900
	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCTGAGCC	1100
60	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150

GATCTGAAGG ACACTATCGC TTCGTTCAAG GCTATCCTGA GCGGTGAGGG 1200
 TGACAGCC 1208

5

2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

	TTCAGGAACT	TATTGTAAGC	CGCCCTCTTT	ATGCATTGAG	GGTGAATAAG	50
	AAGGCTGACA	GGTAATAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	100
	CGTGTTCACT	GGTGTCGGTG	AGCGTACCCG	TGAAGGAAAC	GATCTGTACC	150
25	ATGAAATGCA	GGAAACCCGC	GTCATCCAGC	TTGATGGCGA	GTCTAAGGTC	200
	GCCCTTGTTG	TCGGTCAGAT	GAACGAGCCC	CCTGGAGCCC	GTGCCCCTGT	250
	CGCTCTTACT	GGTCTTACCG	TTGCCGAATA	CTTCCGTGAC	GAGGAGGGCC	300
	AAGATGGTAC	GCCTTTTTTAC	TCTTCTTATT	CTTCGGGTCG	GACTIONACAGAA	350
	CTAACCTGCT	CCAGTGCTTC	TCTTCATTGA	TAACATTTTC	CGTTTTACAC	400
30	AAGCCGGTTC	TGAGGTGTCT	GCCTTGCTTG	GACGTATTCC	CTCTGCCGTC	450
	GGTTACCAGC	CCACTCTCGC	CGTCGACATG	GGTGGTATGC	AGGAACGTAT	500
	CACAACCACC	AACAAGGGTT	CCATTACTTC	CGTG		534

35

2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

	CAAGGCTCAC	GGTGGTTACT	CCGTCTTCAC	TGGTGTCGGT	GAGCGTACCC	50
	GTGAGGGTAA	CGATCTGTAC	CACGAAATGC	AGGAGACCTC	GGTCATTACG	100
	CTCGAGGGCG	AGTCTAAGGT	GGCCCTGGTC	TTTGGTCAGA	TGAACGAGCC	150
55	CCCGGGTGCT	CGTGCCCCTG	TCGCTCTTAC	TGGTCTTACC	GTGCCCAGGT	200
	ACTTCCGTGA	CCAGGAGGGT	CAGGATGGTT	AGTTCTCGTC	CACTCATGCC	250
	GAAACATGTG	CGTGTTCCGA	GGCTAATCAA	CGTGCCAGTG	CTGCTTTTCA	300
	TCGACAACAT	TTTCCGATTC	ACCCAGGCCG	GTTCCGAGGT	GTCTGCCCTG	350
	CTGGGTCGTA	TCCCCTCTGC	CGTCGGTTAC	CAGCCCACCC	TCGCCGTCGA	400
60	CATGGGTGGC	ATGCAGGAGC	GTATCACCAC	CACCAAGAAG	GGCTCTAT	448

2) INFORMATION FOR SEQ ID NO: 896

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

20	ATTCAGGAGC	TGATTGTAAG	TTGCCAATCC	ATGAACTGGA	GATTTGGTGT	50
	GACCCATAGA	ACTAACAAAT	TATTTAGAAC	AACATCGCCA	AGGCTCACGG	100
	TGGTTACTCC	GTCTTCTGTG	GTGTCGGTGA	GCGTACTCGT	GAGGGTAACG	150
	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	TCATCCAGCT	CGAGGGTGAC	200
	TCCAAGGTTC	CTCTGGTCTT	CGGTCAGATG	AACGAGCCCC	CGGGTGCCCG	250
25	TGCCCCGTGC	GCCCTTACCG	GTCTGACCAT	TGCCGAGTAC	TTCCGTGACG	300
	AGGAGGGTCA	GGACGTGCTG	CTCTTCATTG	ACAACATTTT	CCGTTTCACC	350
	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATCC	CCTCTGCCGT	400
	CGGTTACCAG	CCCACTCTGG	CCGTCGACAT	GGGTGGTATG	CAGGAGCGTA	450
	TTACCACCAC	CACCAAGGGT	TCCATTACCT	CCG		483

2) INFORMATION FOR SEQ ID NO: 897

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

50	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTC	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCAGC	CTCTGCTGGC	TTTACCCTC	300
55	GGTGTCAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCAC'TGGT	AAGACCCTCA	550
60	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600

	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCGGC	ATGGTTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
5	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
10	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCC			1124

15 2) INFORMATION FOR SEQ ID NO: 898

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

30	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTTCA	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCCTCTGG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
35	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTT	GTTCCTATCT	CCGGTTTCAA	450
40	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCCCTGG	TACAAGGGTT	500
	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
45	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
	GTTGTACCTT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800
	TGTGCTAACT	TGACACTCAG	CGTCCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
50	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTGCTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTT	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCTTT	1200
55	CCAAGCCCAT	TGTGTGTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTGCT	1250
	TTCGCCGTTT	GCGAGTAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

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2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
20	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
25	TCTGAGGCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAAGTCCCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCACA	GCGTCCTTCC	GACAAGCCCC	600
30	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCGGTGGTAT	CGGAACTGTT	650
	CCTGTCGGCC	GTATCGAGAC	TGGTGTCTTC	AAGCCCGGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
35	CAAGAACGAC	CCCGCTCTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
40	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

60	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
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GTTTCGAGACT CCCAAGTACT ATGTCACCGT CATTGGTACG TCGACTCGCG 100
CGAGACTGGT CGCAATTTCC ACGTCGCTAA CGTGCTTGAA CAGACGCTCC 150
CGGCCACCGT GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG 200
ACTGCGCTAT CCTCATTATC GCTGCCGGCA CTGGTGAGTT CGAGGCTGGT 250
5 ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTGCTCG CCTACACCCT 300
CGGTGTTAAG CAGCTCATCG TCGCTATCAA CAAGATGGAC ACCACCAAGT 350
GGTCTGAGGC CCGTTTCCAG GAGATCATCA AGGAGACCTC CAACTTCATC 400
AAGAAGGTCG GCTACAACCC CAAGACCGTC GCTTTCGTCC CCATCTCTGG 450
TTTCCACGGC GACAACATGC TTTCCCCCTC CACCAACTGC CCCTGGTACA 500
10 AGGGCTGGGA GAAGGAGACC AAGGCTGGCA AGTCCACCGG CAAGACCCTC 550
CTTGAGGCCA TCGACTCCAT CGAGCCCCCC AAGCGCCCCA GCGACAAGCC 600
CCTCCGCCTT CCCCTTCAGG ATGTGTACAA GATCGGCGGT ATCGGCACAG 650
TCCCTGTGCG CCGTATCGAG ACTGGTGTC AAGGCCCCGG CATGGTCGTG 700
ACCTTCGCTC TTCCAACGT CACCACCGAA GTCAAGTCCG TTGAGATGCA 750
15 CCACGAGCAG CTCTCCGAGG GTGTCCCCGG TGACAACGTC GGCTTCAACG 800
TCAAGAACGT CTCCTGCAAG GAGATCCGTC GTGGCAACGT CGCCGGTGAC 850
TCCAAGAACG ACCCCCTCT GGGTGCCGCT TCTTTCGATG CCCAGGTCAT 900
CGTCCTCAAC CACCCCGGCC AGGTGCGTGC TGGCTACGCC CCCGTCCTCG 950
ACTGCCACAC CGCCACATT GCCTGCAAGT TCGCCGAGAT CAAGGAGAAG 1000
20 ATCGACCGCC GTACCGGCAA GTCTGTGCG TCCGCCCCCA AGTTCATCAA 1050
GTCTGGCGAC TCTGCCATCG TCAAGATGAT TCCCTCCAAG CCCATGTGCG 1100
TTGAGGCTTT CACCGACTAC CCTCCTCTGG GCCGCTTCGC CGTCCGTGAC 1150

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2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32075

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

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TACCACTAAG TGGTCCGAGA CCCGATTCAA TGAAATTATC AAGGAAGTCA 50
CCAATTTTCAT TAAGAAGGTC GGATATAACC CCAAGACTGT TCCTTTCGTT 100
CCCATTTTCTG GTTTCGAGGG TGACAACATG ATCGAGCCCT CTGCCAACTG 150
45 CCCATGGTAC AAGGGCTGGT CCAAGGAGAC TGCTCAGGGC AAGTACTCTG 200
GCAAGACCCT TCTTGAGGCC ATCGACGCCA TTGAGCCCCC CACCCGTCCT 250
ACCGATAAAC CTCTCCGTCT TCCCCTCCAG GATGTCTACA AGATCTCCGG 300
TATTGGCACT GTTCTGTGCG GACGTGTTGA GACTGGAGTC ATCAAGCCCG 350
GTATGGTTCGT GACCTTCGCT CCCGCCAACG TCACCACTGA AGTCAAGTCC 400
50 GTCGAAATGC ACCACCAGCA GCTTACCGCC GGTAACCCCG GTGACAACGT 450
CGGCTTCAAC GTCAAGAATG TTTCCGTCAA AGAAGTCCGC CGTGGTAAACG 500
TTGCCGGTGA CTCTAAGAAT GATCCCCCAA AGGGCTGCGA TTCCTTCAAT 550
GCCCAGGTCA TCGTCCTCAA CCACCCTGGT CAGGTTGGCG CTGGTTATGC 600
CCCAAGTCTC GACTGCCATA CTGCCACAT TGCCTGCAA TTCGCTGAGC 650
55 TCCTTGAGAA GATTGATCGA CGAACCGGAA AGTCTGTTGA GAACAACCCC 700
AAGTTCATCA AGTCCGGTGA TGCTGCTATC GTCAAGATGA TTCCTTCCAA 750
G 751

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60

2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

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CGTGAGCGCG GTATCACCAT CGATATTGCT CTGTGGAAGT TCGAGACCCC      50
CAAGTACTAC GTCACCGTCA TTGACGCCCC CGGTCATCGC GATTTCATCA      100
AGAACATGAT CACTGGTACC TCGCAGGCCG ACTGCGCCAT TCTCATCATT      150
GCCGCTGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG ATGGCCAGAC      200
TCGTGAGCAC GCTCTGCTCG CCTACACCCT GGGTGTGCGG CAGCTGATCG      250
TCGCCATCAA CAAGATGGAC ACGGCCAAGT GGGCTGAGGC TCGTTACCAG      300
GAGATCATCA AGGAGACCTC CAACTTCATC AAGAAGGTCG GCTACAACCC      350
CAAGACTGTT GCCTTCGTCC CCATCTCGGG CTTCCACGGC GACAACATGC      400
TTACTCCCTC GACCAACTGC CCCTGGTACA AGGGCTGGGA GAAGGAGGGC      450
AAGAGCGGCA AGGTTACCGG TAAGACTCTG CTGGACGCCA TTGACGCCGT      500
CGAGCCCCCC AAGCGCCCCA CGGACAAGCC CCTGCGTCTG CCCCTCCAGG      550
ATGTCTACAA GATCGGCGGT ATCGGCACTG TCCCTGTCGG CCGTATCGAG      600
ACTGGTGTCC TGAAGCCCCG CATGGTCGTC ACCTTTGCCC CGTCCAACGT      650
CACCCTGAA GTCAAGTCCG TCGAGATGCA CCACGAGCAG CTTGTTGAGG      700
GTGTTCCCGG CGACAACGTC GGCTTCAACG TCAAGAACGT CTCCGTCAAG      750
GAGATCCGTC GTGGCAACGT TGCCGGTGAC TCCAAGAACG ACCCCCCCTC      800
GGGCGCCGCC ACCTTCAACG CCCAGGTCAT TGTCTGAAC CACCCCGGCC      850
AGGTCGGCAA CGGCTACGCC CCGGTTCTGG ACTGCCACAC CGCCACATT      900
GCCTGCAAGT TCACCGAGAT CCTTGAGAAG ATCGACCGCC GTACCGGCAA      950
GTCGGTTGAG AACAACCCCA AGTTCATCAA GTCGGGTGAC GCCGCCATTG     1000
TCAAGCTGAC GCCCTCGAAG CCCATGTGCG TTGAGGCCTT CACTGACTAC     1050
CCCCCT                                           1056

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2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

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CAAGGCTGAG CGTGAGCGTG GTATCACCAT CGATATTGCT CTCTGGAAGT      50
TCCAGACTGC CAAGTACGAG GTTACCGTCA TTGACGCCCC CGGTCACCGT      100
GATTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCCG ATTGCGCTAT      150

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TCTCATCATT GCCTCTGGTA CTGGTGAATT CGAGGCTGGT ATCTCCAAGG      200
ATGGCCAGAC TCGTGAGCAC GCTCTTTTGG CTTTCACCCT CGGTGTCCGT      250
CAGCTCATTG TTGCCCTCAA CAAGATGGAC ACTTGCAAGT GGTCTCAGGG      300
TGAGTACTCG TACCTGCGTT TGGCCTTGAA TATCTTACTA ATGCACCATA      350
5  GATCGTTACA ACGAAATTGT CAAGGAGACT TCCAAC TTCA TCAAGAAGGT      400
CGGATACAAC CCTAAGAACG TTCCTTTCGT TCCTATCTCC GGTTCACACG      450
GTGACAACAT GCTTGAGCCC TCCCCCACT GCCCCTGGTA CAAGGGTTGG      500
GAGAAGGAGA CCAAGGCCGG TAAGGTCACT GGTAAGACCC TCCTCGAGGC      550
CATCGACGCC ATTGAGCCCC CTACCCGTCC CGCCAACAAG GTTAGTCCCT      600
10 CCTCGACTAC TCAAACCCCT CTCATAAGTT CAGATTACTG ACTCGTTCAC      650
AGCCCCCTCCG TCTTCCCCTC CAGGATGTCT ACAAGATCGG TGGTATTGGA      700
ACGGTTCCCG TCGGTCGTGT TGAGACTGGT ACCATCGTTC CTGGTATGGT      750
TGTCACCTTG TAAGTCACTC TCCTCGCTTA TCCTACCTGA AATCATCATG      800
TGCTAACTTG AACTCAGCG CTCCCGCCAA CGTCACCACT GAAGTCAAGA      850
15 GTGTTGAAAT GCACCACCAG GAGCTCACTG CCGGTCAGCC CGGTGACAAC      900
GTTGGTTTCA ACGTGAAGAA CAGTCTCCGT AAGGAAATCC GTCGTGGTAA      950
CGTTGCTGGT GACAGCAAGA ACGACCCCCC TGCCGGTGCT GCCTCCTTCA     1000
ACGCCCAGGT CATCGTCCCT AACCACCCCCG GTCAGGTCGG TGCTGGTTAC     1050
GCCCCAGTCC TCGATTGCCA CACTGCCCCAC ATTGCTTGCA AGTTCGCTGA     1100
20 GCTCCTCGAG AAGATTGACC GTCGTACCGG AAAGTCTGTT GAGGACCACC     1150
CCAAGTTCAT CAAGTCCGGT GACGCTGCCA TCGTCAAGAT GATTCCTTCC     1200
AAGCCCATGT GTGTTGAGGC TTTCACCGAG TACCCTCCTC TCGGTCGTTT     1250
CGCCGTTTCG GAGTAAGTTT TATCTCCGTT GTCTATTTTC CATCCTTCCC     1300
TTCTCCTCCG TCTTCCATAT ATATTTTTTC AGTTATATGT GACTAACCAC     1350
25 AAATCACGGG AATAGC                                     1366

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2) INFORMATION FOR SEQ ID NO: 904

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Curvularia lunata*
 (B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

```

45 CTATTATCGT TGTTGCCGCT TCCGACGGTC AAATGCCCCA GACTCGTGAG      50
CATCTGCTGC TCGCCCGCCA GGTCGGTGTC CAGAAGATCG TTGTCTTCGT      100
CAACAAGGTC GATGCTGTTG AGGACAAGGA GATGTTGGAG CTCGTCGAGA      150
TGGAGATGCG CGAATTGCTC AGCAGCTACG GCTTCGAGGG CGACGAGACT      200
CCCATCATCA TGGGATCTGC CCTCTGCGCC ATTGAGGGCC GCGAACCTGA      250
50 GATTGGTGTC AACC GAATTG ATGAGCTGCT CGAGGCCGTT GATACTTGGA      300
TCCCCACCCC TCAGCGTGAG ACCGACAAGC CTTTCCTCAT GGCCGTCGAG      350
GATGTCTTCT CCATTGCTGG TCGTGGCACT GTCGTCTCTG GCCGTGTCGA      400
GCGAGGTATC CTGAAGCGCG ATGCTGAAGT TGAGCTCGTC GGCAAGGGCA      450
CCGCCCCCAT CAAGACCAAG GTTACCGATA TCGAGACCTT CAAGAAGTCC      500
55 TGCGAGGAGT CTCGCGCTGG TGACAAC TCC TCCCTT TCCTGCTGTT      550
CAAGCGTGAT GAAGTCCGCC GTGGTATGGT CGTTTCCGTC CCTGGACAGG      600
TCAAGGCGCA CAAGAAGTTC CTTGTCTCCA TGTACGTGTT GAGCAAGGAG      650
GAAGGTGGTC GTCACACTGG CTTCCGGTGAG AACTACAGGC CGCAAATGTT      700
CATCCGCACT GCCGACGAGT CGTGTGCCCT GTACTGGCCA GAAGGCACCG      750
60 AGGACGCCCA TGACAAGCTT GTTATGCCCC GTGACAACGT CGAGATGGTT      800

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TGCGAGCTCC ATGCACCACA CGTCTTGGAG CCTGGTCAAC G

841

5 2) INFORMATION FOR SEQ ID NO: 905

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

20 CGGTGCTATC ATTGTCGTCG CCGCCTCCGA CGGTCAGATG TACGTTAACC 50
 TTTAAAGAAT AACTCTCCTT CAGTATATAT GCTTACACTG GCGATCAACA 100
 GGCCCCAGAC TCGTGAGCAC TTGCTGCTTG CTCGTCAGGT CGGTGTCCAG 150
 AAGATCGTTG TCTTCGTCAA CAAGGTCGAT GCTATCGATG ACCCCGAGAT 200
 25 GCTGGAGCTC GTTGAGCTGG AAATGCGCGA GCTTCTCAGC ACCTACGGAT 250
 TCGAGGGTGA GGAGACCCCC ATCGTCTTCG GCTCTGCTCT CTGCGCCATT 300
 GAGGACCGCC GCCCCGACAT CGGTACCGAG CGTATCGACG CTCTCCTCGA 350
 GGCCGTTGAC ACCTGGATCC CCACTCCCCA GCGTGACCTT GACAAGCCTT 400
 TCTTGATGTC CATTGAGGAA GTTTTCTCCA TCCCCGGTCG TGGTACCGTC 450
 30 GCCTCCGGCC GTGTCGAGCG TGGTCTCCTG AAGCGTGATA GCGAGGTTGA 500
 GATCATCGGT ACCACCAACG AGGTCATCAA GACCAAGGTT ACCGACATTG 550
 AGACCTTCAA GAAGTCCTGC TCCGAGTCCC GCGCCGGTGA CAACTCCGGT 600
 CTCCTGCTCC GTGGTGTCCG CCGTGAGGAT CTCCGCCGTG GTATGGTCAT 650
 TGCCGCTCCT GGCAGCGCCA AGGCCAACAG CAAGTTCATG GTCTCCATGT 700
 35 ACGTCCTGAC CGAGGCTGAR GGTGGTCGCC GTACCGGTTT CGGTGTCCAG 750
 TACCGTCCCC AGCTGTTTCT CCGCACTGCC GGTAAGTAAA ATTGCAATTCT 800
 ATTCCGCTAC TAGGGAACCA TCTCTAATTC TATTTGCTAC AGATGAGGCT 850
 GCTGAGTTCA GCTTCCCCGA CGGAGACCAG TCCCGCCGTA TCATGCCCCG 900
 TGACAACGTC GAGATGATCG TCAAGACCCA CCGCCCCGTC GCCGCCGAGG 950
 40 CCGGTCAGCG CTTCAAC 967

2) INFORMATION FOR SEQ ID NO: 906

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

60 TGGTGCTATT ATTGTTGTTG CCGCTTCCGA CGGTCAAATG CCCCAGACTC 50

	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
5	CCCACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCGCT	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
10	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
	GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTTAAG	GCGCACAAGA	AGTTCCCTTG	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
15	CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCCGGTGAC	AACGTCGAGA	800
	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

20

2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCGTCAGG	TCGGTGTCCA	150
40	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCCTGAGA	200
	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TTGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
45	TTCCTCATGT	CTGTGCGAGG	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
	TGCCTCCGGC	CGTGTGCAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500
	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACCTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
50	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTTC	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
55	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
	CTGGCCAGCG	CTTCAA				966

60 2) INFORMATION FOR SEQ ID NO: 908

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

```

15  GGTGCTATCA TCGTCGTTGC TGCTTCCGAT GGTCAGATGC CCCAGACCCG      50
    TGAGCACTTG CTGCTCGCCC GTCAGGTCGG TGTTTCAGAAG ATCGTTGTCT      100
    TCGTCAACAA GGTTCGATGCT GTCGAAGACC CGGAGATGTT GGAACCTCGTC      150
    GAGATGGAGA TGCCTGAGTT ACTCACCAGC TACGGCTTCG AGGGCGACGA      200
20  GACACCCATC ATCATGGGTT CCGCTCTATG CGCCATCGAG GGCCGCCAGC      250
    CCGAGATCGG TGTTACCAAG GTCGACGAGC TAATGGACGC TGTCGACTCA      300
    TGGATCCCCA CCCCTCAGCG TGAGACCGAG AAGCCTTTCC TCATGGCTGT      350
    TGAGGATGTC TTCTCGATTG CTGGACGTGG TACCGTCGTT TCGGGCCGTG      400
    TCGAGCGCGG TATCTTGAAG CGTGACGCTG AAGTCGAGCT TGTCGGCAAG      450
25  GGCACCGCGC CAATCAAGAC CAAGGTCACT GATATTGAGA CCTTCAAGAA      500
    GTCGTGCGAG GAGTCGCGCG CGGGTGATAA CTCCGGTCTT CTCTCCGTG      550
    GTGTCAAGCG TGATGACGTT CGCCGCGGTA TGGTTGTTTC CGTTCCCGGA      600
    CAAGTCAAGG CTCACAAGAA GTTCCTTGTC TCCATGTACG TTCTAAGCAA      650
    AGAGGAGGGT GGTCTGCACA CCGGCTTCGG CGAGAACTAC AGGCCGCAAA      700
30  TGTTTCATCC AACTGCCGAT GAATCCTGCG CACTTCACTT CCCAGAGGGT      750
    ACCGAGGATG CGCACGACAA GCTAGTTATG CCCGGTGACA ACGTCGAGAT      800
    GGTCTGCGAA CTCCACCAGC CCCACGTTCT AGAGACCGGT CAGCG          845
  
```

2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

```

    CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
    AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG      100
    CACTTGCTCC TCGCCCGTCA GGTCCGTGTT CAAAAGATCG TCGTCTTCGT      150
55  CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTGTTCGAAT      200
    TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC      250
    CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA      300
    GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA      350
    TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG      400
60  GAAGTTTCTT CCATCTCTGG TCGTGGTACC GTTGCACTG GTCTGTGTTG      450
  
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GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
5 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
GAAGGTGGTC GTCGTA CTGG ATTCCGGCGCC AACTACCGTC CTCAAGCTTT 750
CATCCGTA CTGG GCTGCTACTC TCAGCTTCCC CCGTGACGAT 800
GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CCGTGACGAT 850
CAGTCCAAGC AGGTCATGCC CCGTGACAAC GTTGAGATGA TCTTGAAGAC 900
10 ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

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2) INFORMATION FOR SEQ ID NO: 910

```

15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 931 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
25 (A) ORGANISM: Penicillium marneffei
    (B) STRAIN: ATCC 58950

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

```

30 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTGCAAT 200
TGGAAATGCG TGAACCTTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
35 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
TCCCCACCCC CCAGCGTGAC CTTGACAAGC CTTTCTTGAT GTCCGTTGAG 400
GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCACTG GTCGTGTTGA 450
GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
40 AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
GAAGGTGGTC GTCGTA CTGG ATTCCGGCGCC AACTACCGTC CTCAAGCTTT 750
45 CATCCGTA CTGG GCTGCTACTC TCAGCTTCCC CCGTGACGAT 800
GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CCGTGACGAT 850
CAGTCCAAGC AGGTCATGCC CCGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

```

50

2) INFORMATION FOR SEQ ID NO: 911

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

5

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

GACGGYSYCA TGCKCAGAC

20

35

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

GAARAGCTGC GGRCGRTAGT G

21

55

2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915
AAACGCCTGA GGRCGGTAGT T 21

10

2) INFORMATION FOR SEQ ID NO: 916

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

25 GCCGAGCTGG CCGGCTTCAG 20

2) INFORMATION FOR SEQ ID NO: 917

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

40 TCGTGCTACC CGTYGCCGCC AT 22

2) INFORMATION FOR SEQ ID NO: 918

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: J01672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

60 AGAGAAGCCT GTCGGCACCG TCTGGTTTGC TTTTGCCACT GCCCGCGGTG 50

AAGGCATTAC CCGGCGGGAT GCTTCAGCGG CGACCGTGAT GCGGTGCGTC 100
 GTCAGGCTAC TGCATATGCA TTGCAGACCT TGTGGCAACA ATTTCTACAA 150
 AACACTTGAT ACTGTATGAG CATAAGTAT AATTGCTTCA ACAGAACATA 200
 TTGACTATCC GGTATTACCC GGCATGACAG GAGTAAAAAT GGCTATCGAC 250
 5 GAAAAACAAAC AGAAAGCGTT GGCGGCAGCA CTGGGCCAGA TTGAGAAACA 300
 ATTTGGTAAA GGCTCCATCA TGCCTTGGG TGAAGACCGT TCCATGGATG 350
 TGGAAACCAT CTCTACCGGT TCGCTTTCAC TGGATATCGC GCTTGGGGCA 400
 GGTGGTCTGC CGATGGGCCG TATCGTCGAA ATCTACGGAC CGGAATCTTC 450
 CGGTAAAACC ACGCTGACGC TGCAGGTGAT CGCCGCAGCG CAGCGTGAAG 500
 10 GTAAAACCTG TGCCTTTATC GATGCTGAAC ACGCGCTGGA CCCAATCTAC 550
 GCACGTAAAC TGGGCGTCGA TATCGACAAC CTGCTGTGCT CCCAGCCGGA 600
 CACCGGCGAG CAGGCACCTG AAATCTGTGA CGCCCTGGCG CGTTCTGGCG 650
 CAGTAGACGT TATCGTCTGT GACTCCGTGG CGGCACTGAC GCCGAAAGCG 700
 GAAATCGAAG GCGAAATCGG CGACTCTCAC ATGGGCCTTG CGGCACGTAT 750
 15 GATGAGCCAG GCGATGCGTA AGCTGGCGGG TAACCTGAAG CAGTCCAACA 800
 CGCTGCTGAT CTTCATCAAC CAGATCCGTA TGAAAATTGG TGTGATGTTC 850
 GGTAACCCGG AAACCACTAC CGGTGGTAAC GCGCTGAAAT TCTACGCCTC 900
 TGTTCTGCTC GACATCCGTC GTATCGGCGC GGTGAAAGAG GGCGAAAACG 950
 TGGTGGGTAG CGAAACCCGC GTGAAAGTGG TGAAGAACAA AATCGCTGCG 1000
 20 CCGTTTAAAC AGGCTGAATT CCAGATCCTC TACGGCGAAG GTATCAACTT 1050
 CTACGGCGAA CTGGTTGACC TGGGCGTAAA AGAGAAGCTG ATCGAGAAAG 1100
 CAGGCGCGTG GTACAGCTAC AAAGGTGAGA AGATCGGTCA GGGTAAAGCG 1150
 AATGCGACTG CCTGGCTGAA AGATAACCCG GAAACCGCGA AAGAGATCGA 1200
 GAAGAAAGTA CGTGAGTTGC TGCTGAGCAA CCCGAACTCA ACGCCGGATT 1250
 25 TCTCTGTAGA TGATAGCGAA GGCCTAGCAG AAATAACGA AGATTTTAA 1300
 TCGTCTTGTT TGATACACAA GGGTCGCATC TGCGGCCCTT TTGCTTTTTT 1350
 AAGTTGTAAG GATATGCCAT GACAGAATCA ACATCCCGTC G 1391

30

2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCIGART CITMIGGIAA RAC

23

45

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

60

2) INFORMATION FOR SEQ ID NO: 921

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

15 TIYRTIGAYG CIGARCAIGC 20

2) INFORMATION FOR SEQ ID NO: 922

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

30 TARAAYTTIA RIGCIYKICC ICC 23

2) INFORMATION FOR SEQ ID NO: 923

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

GACGCIGCCA TCCTGATGAT C 21

2) INFORMATION FOR SEQ ID NO: 924

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

5

2) INFORMATION FOR SEQ ID NO: 925

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

20

2) INFORMATION FOR SEQ ID NO: 926

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

35

2) INFORMATION FOR SEQ ID NO: 927

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

ACGCGGAGAA GGTGCGCTT

19

50

2) INFORMATION FOR SEQ ID NO: 928

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

55

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

GGTCGTTCTT CGAGTCACCG CA

22

10

2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*
 (B) STRAIN: ATCC 25285

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

30 TTCAGCATGC CATTTCAAAA CAGGCCGAAG CCGATATCGT GATTATCGCT 50
 GCTTGTGGGG AGCGTGCAAA TGAAGTTGTG GAAATCTTTA CCGAATTTCC 100
 GGAATTGGTG GACCCGCACA CGGGACGTAA GCTGATGGAG CGTACCATTA 150
 TTATCGCAAA TACATCGAAC ATGCCGGTAG CAGCGCGTGA AGCTTCTGTG 200
 TATACGGCCA TGACGATTGC CGAATACTAT CGTGCCATGG GATTGAAAGT 250
 CCTGCTGATG GCAGACTCCA CTTCCCGTTG GGCGCAGGCA TTGCGTGAGA 300
 TGTCGAACCG TATGGAGGAG TTGCCCGGAC CGGATGCATT CCCGATGGAC 350
 CTGTCTCTAA TCATTTCTAA CTTCTATGGC CGTGCAGGCT ACGTGAAACT 400
 35 GAATAACGGC GAGAGCGGTT CTATTACCTT TATCGGTACA GTATCACC 448

2) INFORMATION FOR SEQ ID NO: 930

40

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 438 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

55 GCTATCTCTA AACAAAGCGGA AGCGGATATC GTGATTATCG CCGCCTGCGG 50
 TGAGCGTGCG AATGAGGTCG TAGAGGTATT TACGGAGTTC CCGGAATTGG 100
 TAGACCCGCA TACGGGACGT AAATTGATGG AACGTACGAT CATTATCGCC 150
 AATACATCCA ACATGCCGGT AGCCGCTCGT GAGGCATCCG TATATACGGC 200
 GATGACCATC GCCGAGTATT ATCGCAGCAT GGGTTTGAAG GTTCTGTTGA 250
 60 TGGCCGACTC TACTTCCCGC TGGGCACAGG CTTTGCCTGA GATGTCCAAC 300

CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
TATCGTGGCG	AACTTCTACG	CTCGTGCGGG	ATTCGTTTCAT	TTGAATAACA	400
ACGCTACAGG	CTCCGTCCT	TTCATCGGTA	CGGTATCG		438

5

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 453 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
25 CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCGG	200
TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
GTACTCCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
30 ACTTGTCGGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
AGC					453

35

2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
55 TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
ACATTCTCTG	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
TCCAAGTCCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
60 CGTGGAACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450

	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
5	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGACGGT	ACTAAATTCT	CTATC		835

10

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

25

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

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2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

GGIAARWSIC ARYTITGYCA YAC

23

55

60 2) INFORMATION FOR SEQ ID NO: 936

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936
TCISIIYTCIG GIARRCAIGG 20

15 2) INFORMATION FOR SEQ ID NO: 937

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937
ATIIACIGARG YITTYGGIGA RTT 23

30 2) INFORMATION FOR SEQ ID NO: 938

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938
CYIGTIGYIS WIGCRTGIGC 20

45 2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1203 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: D10023
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

	ATGTCTCAAG	TTCAAGAACA	ACATATATCA	GAGTCACAGC	TTCAGTACGG	50
	GAACGGTTCG	TTGATGTCCA	CTGTACCAGC	AGACCTTTCA	CAGTCAGTCG	100
5	TTGATGGAAA	CGGCAACGGT	AGCAGCGAAG	ATATTGAGGC	CACCAACGGC	150
	TCCGGCGATG	GTGGCGGATT	GCAGGAGCAA	GCGGAAGCGC	AAGGTGAAAT	200
	GGAGGATGAA	GCATACGATG	AAGCTGCCTT	AGGTTGCTTT	GTGCCAATAG	250
	AAAAACTGCA	AGTGAACGGG	ATTACTATGG	CGGATGTGAA	AAAATAAGG	300
	GAGAGTGGGC	TTCACACTGC	TGAAGCGGTA	GCATATGCTC	CCAGAAAGGA	350
10	TTTATTGGAA	ATCAAAGGTA	TATCGGAAGC	TAAGGCAGAT	AAGTTGCTAA	400
	ACGAAGCGGC	AAGGCTAGTG	CCTATGGGAT	TTGTCACGGC	TGCTGATTTT	450
	CATATGAGAA	GATCGGAGCT	GATTTGTTTG	ACAACGGGTT	CTAAGAATTT	500
	GGACACTCTT	TTGGGTGGTG	GTGTGGAAAC	TGGTTCTATT	ACTGAGCTTT	550
	TCGGTGAATT	CAGGACAGGT	AAGTCCCAGC	TATGTCACAC	TTTGCCCGTG	600
15	ACATGCCAAA	TTCCATTGGA	TATTGGTGGC	GGTGAAGGTA	AGTGTTTGTA	650
	TATCGATACC	GAAGGTACTT	TCAGGCCGGT	AAGATTGGTA	TCCATAGCTC	700
	AGCGGTTTCG	ATTAGACCCG	GATGATGCTT	TGAACAACGT	TGCGTATGCA	750
	AGAGCCTATA	ACGCCGATCA	TCAGTTAAGA	CTTCTGGATG	CTGCTGCCCA	800
	AATGATGAGC	GAGTCTCGGT	TTTCCTTGAT	TGTGGTCGAT	TCTGTTATGG	850
20	CTCTATACCG	TACGGATTTT	TCTGGTCGTG	GTGAACTAAG	CGCAAGGCAA	900
	ATGCATTTAG	CCAAATTTAT	GCGTGCTTTG	CAAAGGCTGG	CCGACCAATT	950
	TGGTGTTGCA	GTCTGCGTTA	CTAACCAAGT	GGTCGCCCAA	GTTGATGGTG	1000
	GTATGGCTTT	TAATCCAGAT	CCAAAGAAGC	CTATCGGTGG	TAATATTATG	1050
	GCACATTCTT	CCACCACGCG	ATTAGGTTTC	AAAAAGGGTA	AGGGATGTCA	1100
25	AAGATTATGC	AAAGTTGTTG	ACTCACCTTG	CTTACCAGAG	GCTGAATGTG	1150
	TGTTGCGGAT	CTATGAAGAT	GGTGTGTTGG	ACCCAGAGA	AGAAGACGAG	1200
	TAG					1203

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2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1800 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
- (B) STRAIN: GRF88
- (C) ACCESSION NUMBER: M87549

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
50	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
55	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
60	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650

	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAAACCT	CTGCTGTAGA	GGTTCTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
5	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGA	AAAATTAAAG	900
	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATAC	TTTGTGTGTT	1100
10	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
15	CAAACCTTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
	CAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
20	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

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DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 2 DE 2

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME OF

NOTE: For additional volumes-please contact the Canadian Patent Office

What is claimed is:

1. A repertory of nucleic acid sequences used for the detection and/or identification of a bacterial, fungal or parasitical species, genus, family or group, which repertory is created by amplifying the nucleic acids of a plurality of determined bacterial, fungal and parasitical species with any combination of the primer pairs shown in annex I, annex II and annex XXI.

2. A nucleic acid used for universal detection of any bacterium, fungus or parasite which is derived from the repertory of claim 1.

A nucleic acid used for universal detection as set forth in claim 2, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any bacterium, fungus or parasite and with any one of SEQ ID NOs: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922.

4. A nucleic acid used for the specific and ubiquitous detection and for identification of a bacterial, fungal or parasital species, genus, family or group, which is derived from the repertory of claim 1.

5. A nucleic acid as set forth in claim 4, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of said bacterial, fungal or parasitical species, genus, family or group and with any one of :

SEQ ID NOs:

630, 629	for the detection and/or identification of <i>Chlamydia pneumoniae</i>
554, 555	for the detection and/or identification of <i>Chlamydia trachomatis</i>
551, 552	for the detection and/or identification of <i>Neisseria gonorrhoeae</i>
549, 550, 627, 625, 628, 626, 582, 583	for the detection and/or identification of <i>Streptococcus agalactiae</i>
576, 632, 631, 633, 634, 635	for the detection and/or identification of <i>Candida</i> spp.
545, 546	for the detection and/or identification of <i>Corynebacterium</i> spp.
656, 657, 271	for the detection and/or identification of <i>Enterococcus</i> spp.
541, 542, 544	for the detection and/or identification of <i>Pseudomonads</i> group

553, 575, 707, 605, 606	for the detection and/or identification of <i>Staphylococcus</i> spp.
547, 548	for the detection and/or identification of <i>Streptococcus</i> spp.
539, 540	for the detection and/or identification of <i>Mycobacteriaceae</i> family
577	for the detection and/or identification of <i>Candida albicans</i>
578	for the detection and/or identification of <i>Candida dubliniensis</i>
580, 603	for the detection and/or identification of <i>Enterococcus faecalis</i>
602	for the detection and/or identification of <i>Enterococcus faecium</i>
604	for the detection and/or identification of <i>Enterococcus gallinarum</i>
579	for the detection and/or identification of <i>Escherichia coli</i>
581	for the detection and/or identification of <i>Haemophilus influenzae</i>
584, 585, 586, 587, 588	for the detection and/or identification of <i>Staphylococcus aureus</i>
589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>
599, 600, 601, 695	for the detection and/or identification of <i>Staphylococcus saprophyticus</i>
for the detection and/or	identification of <i>Enterococcus casseliflavus-flavescens-gallinarum</i>
820, 821, 822	for the detection and/or identification of <i>Trypanosoma brucei</i>
794, 795	for the detection and/or identification of <i>Trypanosoma cruzi</i>
798, 799, 800, 801, 802, 803, 804, 805, 806, 807	for the detection and/or identification of <i>Cryptosporidium parvum</i>
825, 826	for the detection and/or identification of <i>Bordetella</i> spp.
796, 797, 808 809, 810, 811	for the detection and/or identification of <i>Clostridium</i> spp.
703, 704, 705, 706, 793	for the detection and/or identification of <i>Entamoeba</i> spp.
816, 817, 818, 819	for the detection and/or identification of <i>Giardia</i> spp.
701, 702	for the detection and/or identification of <i>Leishmania</i> spp.
823, 824	for the detection and/or identification of <i>Trypanosoma</i> spp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of <i>Kinetoplastidae</i> group
933, 934	for the detection and/or identification of <i>Enterobacteriaceae</i> group

6. A method for the specific detection or identification of a bacterial, fungal or parasitical species, genus, family or group in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claim 4, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific bacterial, fungal or parasitical species, genus, family or group.

7. A method as set forth in claim 6, which is for the detection or identification of bacterial species, genus, family or group.

8. A method as set forth in claim 7, which further comprises probes or primers, or both, for the detection of at least one of the antibiotic resistance genes listed in Table 5.

9. A method as set forth in claim 7 or 8, which further comprises probes or primers, or both, for the detection of at least one of the toxin genes listed in Table 6.

A method as defined in claim 6, which further comprises the universal detection of any species, genus, family or group of bacteria, fungi or parasites.

11. A method as defined in any one of claims 7 to 9, which further comprises the universal detection of any species, genus, family or group of bacteria.

Figure 1: *atpD* sequences databases and main subsets

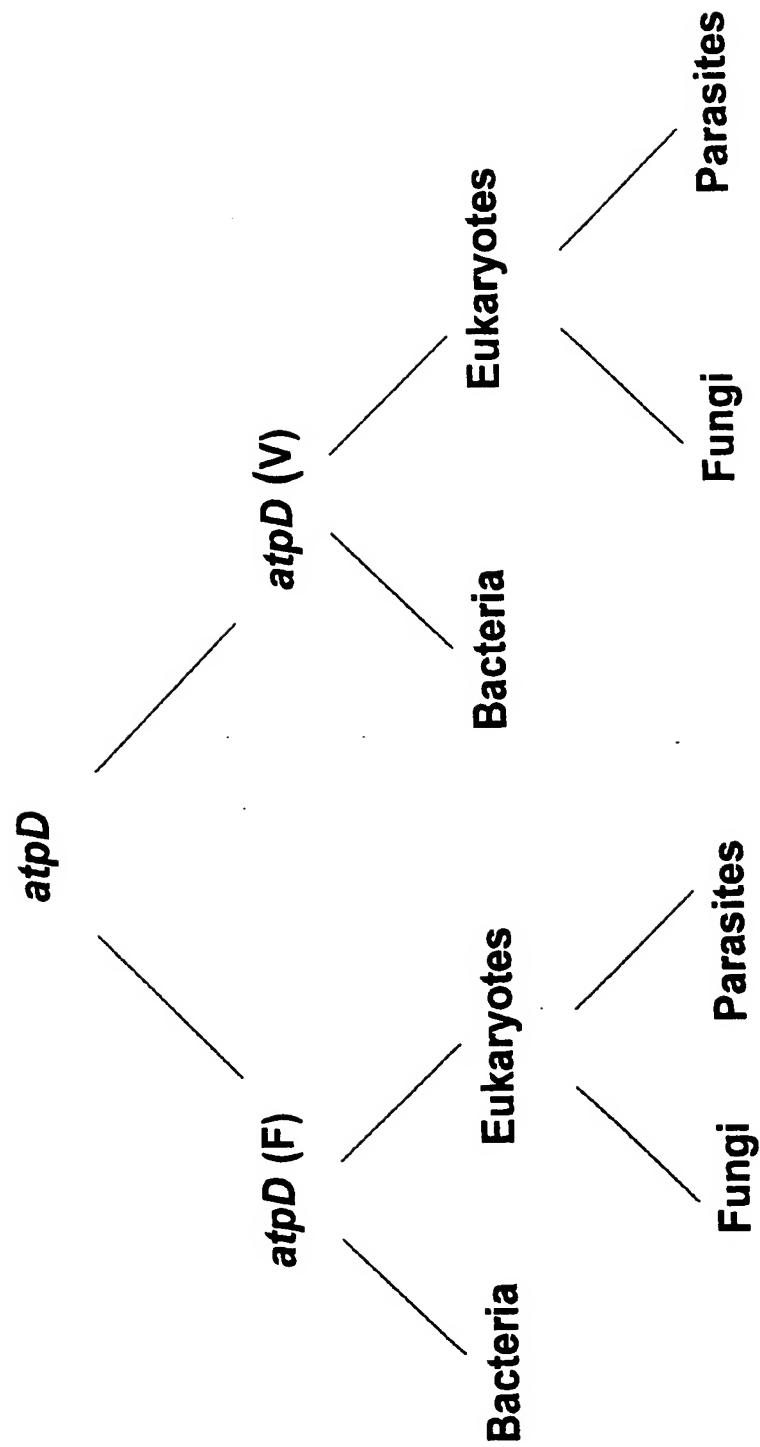


Figure 2: *tuf* sequences databases and main subsets

